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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/030,226	01/08/2002	Noriyuki Morikawa	084335-0154	9242
22428	7590	07/27/2004	EXAMINER	
FOLEY AND LARDNER SUITE 500 3000 K STREET NW WASHINGTON, DC 20007			HAMUD, FOZIA M	
			ART UNIT	PAPER NUMBER
			1647	

DATE MAILED: 07/27/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/030,226

Applicant(s)

MORIKAWA ET AL.

Examiner

Fozia M Hamud

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 29 April 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-4 and 17-28 is/are pending in the application.
- 4a) Of the above claim(s) 19,20 and 24-28 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-4, 17, 18 and 21-23 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 07/02; 01/03.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: sequence alignment.

DETAILED ACTION

Election/Restriction:

1a. Originally, claims 1-16 have been filed, of which claims 5-16 have been cancelled and claims 1 and 2 have been amended. New claims 17-28 have been added. The latest list of claims, filed on 29 April 2004, do not list claims 3 and 4. However, since claims 3 and 4 have never been cancelled, these claims will be considered as pending. Thus claims 1-4, 17-28 are pending.

1b. Applicant's election of the invention of Group I (original claims 1-6 and 9-11) filed on 29 April 2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)). Claims 1-4, 17, 18, 21-23 are drawn to the elected invention and are under consideration.

The restriction requirement is still deemed proper and is therefore made FINAL.

Claims 19, 20, 24-28 are withdrawn from consideration by the Examiner as they are drawn to non-elected inventions.

Priority:

2a. The subject matter claimed in the instant application is afforded the filing date of the current application, which is 08 January 2002. The claimed nucleic acid encodes the polypeptide of SEQ ID NO:2, which is described as being a fatty acid transport protein. Example 5 of the instant specification demonstrates that oleic acid incorporation by cells expressing the protein of the instant invention was significantly enhanced, thus

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satisfying the requirements under 35 USC § 112 of how to make and the use the claimed invention.

Should the applicants disagree with the examiner's factual determination above, it is incumbent upon the applicants to provide the serial number(s) and specific page number(s) of any parent application filed prior to 01/08/02, which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 01/08/02. Applicants must also provide translations of such documents when necessary.

Amendment to the Specification:

3a. The amendment filed on 08 January 2002 and resubmitted on 29 April 2004 is improper because it does not conform to 37 CFR 1.121 which requires that the location and sections of the specification that changes are made to must unambiguously be identified, for example, any additions may be underlined and any deletions may be enclosed in brackets. In the instant case the amendment does not identify what is being added or deleted from the sections of the specification that is supposed to be amended. Appropriate correction is requested.

2b. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code on page 4, lines 10, 17, 19, 23 and on pages 7 and 19. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Information Disclosure:

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3a. A copy of the reference by J.E Schaffer (Circulation, vol.96, No.8) has not been submitted by Applicants and an attempt to obtain said document has not been successful. Applicants are kindly requested to provide a copy of this reference.

Claim rejections-35 USC § 112:

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4a. Claims 1-4, 17, 18 and 21-23 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide comprising the nucleotide sequence set forth in SEQ ID NO:1, said polynucleotide encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, an expression vector comprising said polynucleotide and a method of producing the encoded protein, does not reasonably provide enablement for an isolated polynucleotide which encodes a protein that comprises the amino acid sequence set forth in SEQ ID NO:2, wherein one or more amino acids have been substituted, deleted, inserted and/or added, or which has over all mutations that is 10% or less; or an isolated nucleic acid which encodes a functional equivalent to the protein of SEQ ID NO:2; or encodes a partial protein. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The instant specification describes the polypeptide of SEQ ID NO:2 as a fatty acid transport protein and demonstrates that oleic acid incorporation by cells expressing

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the protein of the instant invention was significantly enhanced (see example 5).

However, the instant specification does not disclose any polypeptide wherein one or more amino acids have been substituted, deleted, inserted and/or added, or which has over all mutations that is 10% or less that retain the activity of the polypeptide of SEQ ID NO:2. Neither does the instant specification disclose any "functional equivalents" of the polypeptide of the instant invention. Support for "functional equivalents" is found on page 9, lines 29-35, where it states that "functional equivalents" are isolated from rabbits, chickens, however, there is no disclosure of any "functional equivalents" that have the same activity as the polypeptide of SEQ ID NO:2. Applicants do not teach which 10% of the polypeptide of SEQ ID NO:2 to mutate, or which regions of the polypeptide of SEQ ID NO:2 can tolerate deletions, insertions or substitutions of at least one amino acid, without affecting the activity of said polypeptide. Applicants also do not disclose "functional equivalents" of the polypeptide of SEQ ID NO:2 that retain the activity of the polypeptide. Thus without information regarding which regions of the polypeptide of SEQ ID NO:2 are critical to a specific function, the full scope of the claimed invention is not enabled. In summary, the amount of experimentation required for one of ordinary skill in the art to make and use an isolated nucleic acid which encodes a polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:2, wherein one or more amino acids have been substituted, deleted, inserted and/or added, or which has over all mutations that is 10% or less; or an isolated nucleic acid which encodes a functional equivalent to the protein of SEQ ID NO:2; or encodes a partial protein would be undue. In *Ex parte Forman*, 230 USPQ 546 (Bd. Pat. Appls,

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and Interf. 1986), the Board considered the issue of enablement in molecular biology. The Board held that the following factors should be considered to determine whether the claimed invention would require of the skilled artisan undue experimentation: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art and (8) the breadth of the claims. In the instant application, Applicants only disclose one polypeptide, said polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, encoded by the nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO:1, and it will be undue experimentation to delineate "all" possible polypeptides that contain one or more amino acid substitutions, deletions, insertions and/or additions, or which has an overall mutations that is 10% or less; a partial peptide of SEQ ID NO:2 or a functional equivalent to the protein of SEQ ID NO:2 which retain the desired activity, because Applicants have not taught which amino acid residues of SEQ ID NO:2 to alter without altering the desired activity. Furthermore, the state of the art is such that it is acknowledged that amino acid modifications of proteins is unpredictable, thus one of ordinary skill in the art would not be able to predict which amino acids to delete or to substitute while still preserving the desired activity. Neither has the specification disclosed where of the polypeptide of SEQ ID NO:2 to insert amino acids without altering the desired activity. There is no upper limit as to how many amino acids to be substituted, deleted, or inserted or which regions of the polypeptide are critical for its'

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function, the skilled artisan would not know how to make and use the claimed polypeptide. Therefore, the instant specification is only enabling for an isolated nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO:1, said nucleic acid encoding the polypeptide of SEQ ID NO:2.

3b. Claims 1-4, 17-18, 21-23 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention.

The instant specification as filed also only describes the structure of the nucleic acid of SEQ ID NO:1 encoding the polypeptide of SEQ ID NO:2, and fails to describe nucleic acid molecules encoding: functional equivalents, or polypeptide that contain one or more amino acids substitutions, deletions, insertions and/or additions, or which has an over all mutations that is 10% or less; partial peptide of SEQ ID NO:2 or a functional equivalent to the protein of SEQ ID NO:2. Therefore, conception is not achieved until reduction to practice has occurred. Adequate written description requires more than a mere statement that it is part of the invention.

To satisfy the written description requirement, an applicant's specification must reasonably convey to those skilled in the art that the applicant was in possession of the claimed invention as of the date of invention. *Regents of the University of California v. Eli Lilly & Co.*, 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1405 (Fed. Cir. 1997); *Hyatt v. Boone*, 146 F.3d 1348, 1354, 47 USPQ2d 1128, 1132 (Fed. Cir. 1998). Furthermore, In *The Regents of the University of California v. Eli Lilly* (43 USPQ2d 1398-1412), the

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court held that a generic statement which defines a genus of nucleic acids by only their functional activity does not provide an adequate written description of the genus.

Adequate written description requires more than a mere statement that it is part of the invention. The court indicated that while Applicants are not required to disclose every species encompassed by a genus, the description of a genus is achieved by the recitation of a representative number of DNA molecules, usually defined by a nucleotide sequence, falling within the scope of the claimed genus. At section B(1), the court states that "An adequate written description of a DNA...requires a precise definition, such as by structure, formula, chemical name, or physical properties', not a mere wish or plan for obtaining the claimed chemical invention". In the instant case, Applicants are claiming nucleic acids encoding variants and fragments of the polypeptide of SEQ ID NO:2, however, Applicants do not provide the structure of any said variants or fragments.

Therefore only the nucleic acid encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, but not the full breadth of the claims, meets the written description provision of 35 U.S.C. 112, first paragraph.

Claim Rejections - 35 U.S.C. § 112, second paragraph:

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claims 1-4, 17-18, 21-23 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

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4a. Claim 1 recites "...wherein overall percentage of mutations is typically 10% or less...", however, it is unclear how much less than 10%, should said mutation be, 5%, 1% or 9.9%? Furthermore, "typically" is a vague term and it renders the claim indefinite.

4b. Claim 1 recites "... In which one or more amino acids have been deleted, substituted, inserted and/or added...", however it is unclear how many amino acids of the polypeptide of SEQ ID NO:2 to delete, insert or substitute for. There is no upper limit as to how many amino acids to alter, is it only one, ten or more? The metes and bounds of the claim cannot be ascertained.

4c. Claim 1 recites "... polynucleotide that hybridizes under stringent conditions...", however, "stringent conditions" is a conditional term and renders the claim indefinite. This rejection could be obviated by supplying specific conditions supported by the specification, which Applicants consider to be "stringent".

4d. Claims 21-23 recite ".....or to a complementary strand thereof", however, it is unclear whether "a complement strand thereof" is to the nucleic acid of SEQ ID NO:1 or to the complement of the nucleic acid of claim 1. Also in claim 21, it is redundant to recite "15 nucleotides" twice in the claim. Furthermore, it appears that claims 21 and 22 are drawn to a subject matter that is of equal scope. Clarification is required.

Claims 2-4, 17-18 are also rejected under 35 U.S.C. § 112, second paragraph, as being indefinite, so long as they depend from claim 1, for the limitations set forth directly above.

Claim rejections-35 USC § 102:

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

5a. Claims 1-4, 17-18, 21-23 are rejected under 35 U.S.C § 102(b) as being anticipated by (WO 99/46281 published 16 September 1999; WO 0053754 published 14 September 2000.

Each of these references teaches an isolated nucleic acid molecule comprising a nucleotide sequence that shares 100% identity to the coding region of the nucleic acid of SEQ ID NO:1 of the instant application and encodes a polypeptide that shares 100% identity to the polypeptide of SEQ ID NO:2 of the instant application. (See attached copy of the comparison of SEQ ID NOs: 1 and 2 of the instant invention and the sequences of the references (SEQUENCE COMPARISON 'A-D'). The references also teach a vector comprising said nucleic acid, a host cell comprising said vector, a method of producing the encoded polypeptide and a probe that is comprises at least 15 nucleotides that is complementary to the nucleic acid of SEQ ID NO:1. Therefore each of the references anticipates the instant claims 1-4, 17-18, 21-23 in the absence of any evidence to the contrary.

5b. Claims 1-4, 17-18, 21-23 are rejected under 35 U.S.C § 102(b) as being anticipated by Hirsch et al (1998).

Hirsch et al disclose an isolated nucleic acid that encodes a fatty acid transporter protein, a vector comprising said nucleic acid, a host cell comprising said vector and a method of producing the encoded polypeptide. The polypeptide disclosed by Hirsch et al shares 54.7% overall homology to the polypeptide of SEQ ID NO:2 of the instant application. (See attached copy of the comparison of SEQ ID NO:2 of the instant

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invention and the sequences of the references (SEQUENCE COMPARISON 'E')..

Therefore, a complement of the nucleic acid encoding the polypeptide disclosed by Hirsch et al would be expected to hybridize to the instant nucleic acid of SEQ ID NO:1, thus anticipating instant claim 1. The nucleic acid encoding the polypeptide disclosed by Hirsch et al would also be expected to contain at least 15 contiguous nucleotides of the instant SEQ ID NO:1, thus meeting the limitations recited in instant claims 21-23. therefore, the Hirsch et al reference anticipates the instant claims 1-4, 17-18, 21-23 in the absence of any evidence to the contrary.

Conclusion:

No claim is allowed.

Advisory Information:

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Fozia M Hamud whose telephone number is (571) 272-0884. The examiner can normally be reached on Monday, Thursday-Friday, 6:00 am to 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda G Brumback can be reached on (571) 272-0961. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

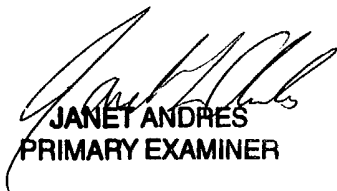
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Fozia Hamud
Patent Examiner
Art Unit 1647
22 July 2004



JANET ANDRES
PRIMARY EXAMINER

Db 421 AGCGCGCGCGCACACCTTTCTCATTCACGCGCTCGCGCGCTTTAGCTACTCAGAGAGCGG 480
Qy 489 AGCGCGAGATACAGAGGCTGACAGCGGCTTCTTACGTGCTTAGGCTGGGACTGGAGAC 548
Db 481 AGCGCGAGATACAGAGGCTGACAGCGGCTTCTTACGTGCTTAGGCTGGGACTGGAGAC 540
Qy 549 CCGACGCGCGCGCACAGCGCGGAGGCGGCTGAGAGAGCGGCGGAGCGGCGGCGGAG 608
Db 541 CCGACGCGCGCGCACAGCGCGGAGGCGGCTGAGAGAGCGGCGGAGCGGCGGCGGAG 600
Qy 609 CCGGAGATGACAGCGCGGAGAGCGGAGGCTTGGCGGAGGAGAGCGGCGGCGGAG 668
Db 601 CCGGAGATGACAGCGCGGAGAGCGGAGGCTTGGCGGAGGAGAGCGGCGGCGGAG 660
Qy 669 GTGAGAGAGCGCGCGGCTTCTGACCTGAGAGCACTGAGCGGCTCTTCCCGCTG 728
Db 661 GTGAGAGAGCGCGCGGCTTCTGACCTGAGAGCACTGAGCGGCTCTTCCCGCTG 720
Qy 729 GCCCAGAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
Db 721 GCCCAGAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 789 TGCCCAACGCGCTGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848
Db 781 TGCCCAACGCGCTGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 849 CGCTGCTGCTGCGCGGAGGTTTCTGAGTCTTGAAGCTTGAAGCTTGAAGCTTGAAG 908
Db 841 CGCTGCTGCTGCGCGGAGGTTTCTGAGTCTTGAAGCTTGAAGCTTGAAGCTTGAAG 900
Qy 909 CCGAGGAGGCTGACCTGAGGAGCTGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 968
Db 901 CCGAGGAGGCTGACCTGAGGAGCTGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 960
Qy 969 TGCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028
Db 961 TGCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 1029 AGAGCAATACAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
Db 1021 AGAGCAATACAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 1089 CTGCTCGAGATCAGTCTGTAAGATCTGCAATGCTGCAATGCTGCAATGCTGCAAT 1148
Db 1081 CTGCTCGAGATCAGTCTGTAAGATCTGCAATGCTGCAATGCTGCAATGCTGCAAT 1140
Qy 1149 TCCACACAGAGAGATGATCTTACCTGCGCTTCCCACTTACCAATGCTGCGCTGCTG 1208
Db 1141 TCCACACAGAGAGATGATCTTACCTGCGCTTCCCACTTACCAATGCTGCGCTGCTG 1200
Qy 1209 TGGGCACTGCTGAGGCTGACATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1268
Db 1201 TGGGCACTGCTGAGGCTGACATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1260
Qy 1269 CTGCTCAGTTCTGAGAGATGCTGAGAGCAAGGCTGAGGCTGAGGCTGAGGCTGAG 1328
Db 1261 CTGCTCAGTTCTGAGAGATGCTGAGAGCAAGGCTGAGGCTGAGGCTGAGGCTGAG 1320
Qy 1329 AGCTGTGCGATACCTTGTCAACAGCGGCGGCGGAGAGGAGGAGGAGGAGGAGGAG 1388
Db 1321 AGCTGTGCGATACCTTGTCAACAGCGGCGGCGGAGAGGAGGAGGAGGAGGAGGAG 1380
Qy 1389 GAGTGGCAGTGGGCGAGCGGCTGCGCCAGATACCTGAGAGCGGCTTGTGCGCGCTG 1448
Db 1381 GAGTGGCAGTGGGCGAGCGGCTGCGCCAGATACCTGAGAGCGGCTTGTGCGCGCTG 1440
Qy 1449 GAGCTGTGAGGCTGCTGAGAGCATGATGATGATGATGATGATGATGATGATGAT 1508
Db 1441 GAGCTGTGAGGCTGCTGAGAGCATGATGATGATGATGATGATGATGATGATGAT 1500
Qy 1509 ACACAGAGCAGAGGCGGCTGCTGAGGAGGCTTCTGCTGCTTACAGAGATCTTCCCT 1568
Db 1501 ACACAGAGCAGAGGCGGCTGCTGAGGAGGCTTCTGCTGCTTACAGAGATCTTCCCT 1560

Qy 1569 TCTCTTGTATTCGCTATGATGTCAACAACAGAGAGGCCAATTCGGGACCCCGAGGCGACT 1628
Db 1561 TCTCTTGTATTCGCTATGATGTCAACAACAGAGAGGCCAATTCGGGACCCCGAGGCGACT 1620
Qy 1629 GATAGGCAATCTCCAGGTAGAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1688
Db 1621 GATAGGCAATCTCCAGGTAGAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Qy 1689 CATTCCTGAGCTATGCTGCGCGGCGAGAGCTGCGCCAGGAGGAGGAGGAGGAGGAG 1748
Db 1681 CATTCCTGAGCTATGCTGCGCGGCGAGAGCTGCGCCAGGAGGAGGAGGAGGAGGAG 1740
Qy 1749 TCCGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1808
Db 1741 TCCGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Qy 1809 TCTCTCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1868
Db 1801 TCTCTCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Qy 1869 CAACCGAGGTGCGAGAGGCTTTCAGAGGCGCTGAGATTTTCTCAGAGGTGAGACGCTAT 1928
Db 1861 CAACCGAGGTGCGAGAGGCTTTCAGAGGCGCTGAGATTTTCTCAGAGGTGAGACGCTAT 1920
Qy 1929 GAGTCACTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1988
Db 1921 GAGTCACTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Qy 1989 CCGACGCTTGTGAGCCTTATGAGCCTTATGAGCCTTATGAGCCTTATGAGCCTTATGAG 2048
Db 1981 CCGACGCTTGTGAGCCTTATGAGCCTTATGAGCCTTATGAGCCTTATGAGCCTTATGAG 2040
Qy 2049 CCGGCGCGCGGAGTCTTCTGAGGCTGCGAGAGCTGCTGAGGAGGAGGAGGAGGAGGAG 2108
Db 2041 CCGGCGCGCGGAGTCTTCTGAGGCTGCGAGAGCTGCTGAGGAGGAGGAGGAGGAGGAG 2100
Qy 2109 AGAAAGTTGAGATGAGCAATGAGGAGGCTTGCAGCCCGAGCACTCTGCTGAGCCACTG 2168
Db 2101 AGAAAGTTGAGATGAGCAATGAGGAGGCTTGCAGCCCGAGCACTCTGCTGAGCCACTG 2160
Qy 2169 TTCTGTGACCAAGCTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2228
Db 2161 TTCTGTGACCAAGCTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2229 TGGCAGAGAACTTGTGAGATCTGAGAACTTGCACACTGAGGAGCCTGAGAGAGAACT 2288
Db 2221 TGGCAGAGAACTTGTGAGATCTGAGAACTTGCACACTGAGGAGCCTGAGAGAGAACT 2280
Qy 2289 GTGGGCTGGGCGGCTTGTGAGAGGATGATGAGGCTGATGAGGAGGAGGAGGAGGAG 2348
Db 2281 GTGGGCTGGGCGGCTTGTGAGAGGATGATGAGGCTGATGAGGAGGAGGAGGAGGAG 2340
Qy 2349 GCGGTCACTATTTGTGATTAATGAGGCTGAGGCTGATGAGGCTGATGAGGCTGATGAG 2400
Db 2341 GCGGTCACTATTTGTGATTAATGAGGCTGAGGCTGATGAGGCTGATGAGGCTGATGAG 2392

RESULT 5
AAZ33977
ID AAZ33977 standard; cDNA; 2574 BP.
XX AAZ33977;
XX 07-DEC-1999 (first entry)
XX
XX Human PRO703 nucleotide sequence.
XX
XX Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein; ss.
XX Homo sapiens.

Sequence
Comparison
'A'

Sequence Comparison

QY	318	TGTGCTGCAAAAGGGCTCTTGAGATCGCGCCCTGGCCGCGCGCTGGCCGCAACCCGAG	377
Db	374	TGTGCTGCAAAAGGGCTCTTGAGACTCGCGCCCTGGCCGCGCGCTGGCCGCAACCCGAG	433
QY	378	GTCCCGAGGGGGGCTGCAAGCTTGGCGCTCTCGCGAATCGGCGCCAGCGCGCCG	437
Db	434	GTCCCGAGGGGGGCTGCAAGCTTGGCGCTCTCGCGAATCGGCGCCAGCGCGCGCCG	493
QY	438	CGACACCTTTCTCAATCAACGGCTCGCGGCCCTTTAATCTACAGAGGGGAGCCGAG	497
Db	494	CGACACCTTTCTCAATCAACGGCTCGCGGCCCTTTAATCTACAGAGGGGAGCCGAG	553
QY	498	GTAAACAGGGCTGCAAGCGCTTCTTACGTGGCTAAGCTTGGAACTTGGGAACTCCACGCG	557
Db	554	GTAAACAGGGCTGCAAGCGCTTCTTACGTGGCTAAGCTTGGGAACTTGGGAACTCCACGCG	613
QY	558	GGCAGACGGCGAGGAGGAGCGCTGGAGAGCGCAGCGGGAGCGCGGAGCCGAGATG	617
Db	614	GGCAGACGGCGAGGAGGAGCGCTGGAGAGGCGCAGCGGGAGCGCGGAGCCGAGATG	673
QY	618	CAGCGGCGCGAAGCGCGCGCGAGTTTGGCGAGGGGAACGTGGCGGCAAGAGTGGAGAG	677
Db	674	CAGCGGCGCGAAGCGCGCGCGAGTTTGGCGAGGGGAACGTGGCGGCAAGAGTGGAGAG	733
QY	678	CGCGCCCGCTCTGATCACTGTAGCAATGTGGGCTGCTCTCCCGCGCTGGCCAGAGT	737
Db	734	CGCGCCCGCTCTGATCACTGTAGCAATGTGGGCTGCTCTCCCGCGCTGGCCAGAGT	793
QY	738	TTCTGTGGCTCTGGTTCCGGGCTGGCCAAAGGCGGCGCTGGCAATGGCTTTGTGCCACG	797
Db	794	TTCTGTGGCTCTGGTTCCGGGCTGGCCAAAGGCGGCGCTGGCAATGGCTTTGTGCCACG	853
QY	798	CCCTGGCGGGGGCCCGCTGCTGCACTGCTCCGACACTCGGCGCGCGCGCTGGCTG	857
Db	854	CCCTGGCGGGGGCCCGCTGCTGCACTGCTCCGACACTCGGCGCGCGCGCTGGCTG	913
QY	858	TGGCGGCAAGTTTCTGGAATCCCTGGAGCCCGACCTGGCCCGGCGTGAAGAGCATAGGGC	917
Db	914	TGGCGGCAAGTTTCTGGAATCCCTGGAGCCCGACCTGGCCCGGCGTGAAGAGCATAGGGC	973
QY	918	TCCACTGTGGCTGAGGCCCGAGAACCCACCTGTGGAATTAACGATTTGCTGGCTG	977
Db	974	TCCACTGTGGCTGAGGCCCGAGAACCCACCTGTGGAATTAACGATTTGCTGGCTG	1033
QY	978	AAGTGTCCGCTGAAGTGAATGGGCGCAGGCGCAGATACCTCTTTCCCGCAGACATTA	1037
Db	1034	AAGTGTCCGCTGAAGTGAATGGGCGCAGGCGCAGATACCTCTTTCCCGCAGACATTA	1093
QY	1038	CAGACAGTGCCTGTACAATTTCACCTCTGGCACAAGGGCCCTCCCAAGAGCTGTCGGA	1097
Db	1094	CAGACAGTGCCTGTACAATTTCACCTCTGGCACAAGGGCCCTCCCAAGAGCTGTCGGA	1153
QY	1098	TCAGTCAATGAAGATCCGCAATGGCAATGGCAGGGCTTATCAGCTGTGTGTGCCACAGG	1157
Db	1154	TCAGTCAATGAAGATCCGCAATGGCAATGGCAGGGCTTATCAGCTGTGTGTGCCACAGG	1213
QY	1158	AAGATGTATCTACTCGCGCCCTCCACTTACCAATGCATGTCGGTCCCTGCTGGCAATG	1217
Db	1214	AAGATGTATCTACTCGCGCCCTCCACTTACCAATGCATGTCGGTCCCTGCTGGCAATG	1273
QY	1218	TGGGCTGCAATGGGCAATGGGGGCAACAGTGGTGGAAATCAAGTTCTGGGCTGGTCAAGT	1277
Db	1274	TGGGCTGCAATGGGCAATGGGGGCAACAGTGGTGGAAATCAAGTTCTGGGCTGGTCAAGT	1333
QY	1278	TCTGGAGATTTGCCAGGACACAGAGGTGACGAGTTTCCAGTACATTGGGAGACTGTGCC	1337
Db	1334	TCTGGAGATTTGCCAGGACACAGAGGTGACGAGTTTCCAGTACATTGGGAGACTGTGCC	1393
QY	1338	GATACCTTGTCAACAGCGCCCGAGCAGAGGAGAACTGTGCCTAATAGTCCGGCTGGAG	1397
Db	1394	GATACCTTGTCAACAGCGCCCGAGCAGAGGAGAACTGTGCCTAATAGTCCGGCTGGAG	1453
QY	1398	TGGGACGGCGGCTGGCCCAATCTCTGGAGCGTTTTGTGGCGCGCTTGGGCGCCCTGCG	1457

Db	1454	TCGGCAGGGGGCTGGGCCAGATACCTGGGAGCGTTTGTGGGGCGCTTCGGGCCCTCGC	1513
QY	1458	AGGTGCTGGAGACATATGGAATGACAGAGGGCAAGTGGCCACCTCAACTACACAGAC	1517
Db	1514	AGGTGCTGGAGACATATGGAATGACAGAGGGCAAGTGGCCACCTCAACTACACAGAC	1573
QY	1518	AGCGGGGCGCTGTGGGGGCTGCTCTCGGCTTACAGATATCTTCCCTCTCTCTGA	1577
Db	1574	AGCGGGGCGCTGTGGGGGCTGCTCTCGGCTTACAGATATCTTCCCTCTCTCTGA	1633
QY	1578	TTTCGTATGATGTCACCAAGAGAGCAATTCGGGACCCCGAGGGGACGTATGAGCA	1637
Db	1634	TTTCGTATGATGTCACCAAGAGAGCAATTCGGGACCCCGAGGGGACGTATGAGCA	1693
QY	1638	CATCTTCAGAGTGAAGCCAGGGCTGTGGTGGCCCCGGTAAAGCAGAGATCCCATTTCTGG	1697
Db	1694	CATCTTCAGAGTGAAGCCAGGGCTGTGGTGGCCCCGGTAAAGCAGAGATCCCATTTCTGG	1753
QY	1698	GCTATGCTGGGGGGCCAGAGCTGGCCCCAGGGGAAAGTTGTAAGGATGCTTCCGGGCTG	1757
Db	1754	GCTATGCTGGGGGGCCAGAGCTGGCCCCAGGGGAAAGTTGTAAGGATGCTTCCGGGCTG	1813
QY	1758	GGGATGTTTTCTTCAACACTGGGGACCTGTGCTCGCATGATGACCAAGATTTTCTCGCT	1817
Db	1814	GGGATGTTTTCTTCAACACTGGGGACCTGTGCTCGCATGATGACCAAGATTTTCTCGCT	1873
QY	1818	TCCATGATGTCATCTGGAGACCTTTCAAGGTGAGAGGGGGGAGATGTCGCACAAACGAG	1877
Db	1874	TCCATGATGTCATCTGGAGACCTTTCAAGGTGAGAGGGGGGAGATGTCGCACAAACGAG	1933
QY	1878	TGCGAGAGGCTTCGAGGGCCCTAGATTTTCTCAGAGGTGAGCGTATGGAATCACTG	1937
Db	1934	TGCGAGAGGCTTCGAGGGCCCTAGATTTTCTCAGAGGTGAGCGTATGGAATCACTG	1993
QY	1938	TGCGAGGGGATGAAGAGCAGGGCTGGAGATGACACCCCTAGTTCTGGGTCCCCCAGCGTT	1997
Db	1994	TGCGAGGGGATGAAGAGCAGGGCTGGAGATGACACCCCTAGTTCTGGGTCCCCCAGCGTT	2053
QY	1998	TGACCTTATGACAGCTTACACCCACGTGTCTGAGAACTTGGCACTTATGCCCCGCC	2057
Db	2054	TGACCTTATGACAGCTTACACCCACGTGTCTGAGAACTTGGCACTTATGCCCCGCC	2113
QY	2058	GATTCCTCAGGCTCCAGAGCTTTTGGCCACACAGACCTTCAAAACGACGAAAGTTC	2117
Db	2114	GATTCCTCAGGCTCCAGAGCTTTTGGCCACACAGACCTTCAAAACGACGAAAGTTC	2173
QY	2118	GGATGGCAATGAGGGCTTGAACCCACGACACCTGTCTGAACCACTGATGCTTCTGACC	2177
Db	2174	GGATGGCAATGAGGGCTTGAACCCACGACACCTGTCTGAACCACTGATGCTTCTGACC	2233
QY	2178	AGGCTGTAGAGTCCATCTGGCCCTCAACTCCCGGTACAGAGCCCTCGGACGAGA	2237
Db	2234	AGGCTGTAGAGTCCATCTGGCCCTCAACTCCCGGTACAGAGCCCTCGGACGAGA	2293
QY	2238	ACCTTGGATCTGAGAACTTCCACCTTGAGGACCTTGAGAGGAACTCTGTGGGGTGG	2297
Db	2294	ACCTTGGATCTGAGAACTTCCACCTTGAGGACCTTGAGAGGAACTCTGTGGGGTGG	2353
QY	2298	GGGCGCTGGAGGTGATCTGGGCTGTCAAGGACCTTTTCTATACAGAACTCGCTCACT	2357
Db	2354	GGGCGCTGGAGGTGATCTGGGCTGTCAAGGACCTTTTCTATACAGAACTCGCTCACT	2413
QY	2358	ATTTTGTATTAATATGCTGCTGAGAGCTGATTCAGACTCTCTGAACCTA 2404	
Db	2414	ATTTTGTATTAATATGCTGCTGAGAGCTGATTCAGACTCTCTGAACCTA 2460	

RESULT 6
AAC78481
ID AAC78481 standard; cDNA; 2574 BP
XX
AC AAC78481;

RESULT 1
ID AAY41699 standard; protein; 730 AA.
AC AAY41699;
XX 07-DEC-1999 (first entry)
DT Human PRO703 protein sequence.
DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridization;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein.
OS Homo sapiens.
PN WO9946281-A2.
PD 16-SEP-1999.
PF 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-00774502.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078935P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 01-APR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.

Sequence Comparison

Claim 12; Fig 39; 530P; English.
The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA23891 to AA23438, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention

Sequence 730 AA;

Query Match 100.0%; Score 3843; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	MGVQRTAPWKEKSOUEERAAAGFRKGGSGMPSGNNQYPTREASMAALLPILILL	60
1	MGVQRTAPWKEKSOUEERAAAGFRKGGSGMPSGNNQYPTREASMAALLPILILL	60
61	PLILKILHWPOLRMLPADIAFAVRALCCERARARALAAADPRGEGCSIAWRIA	120
61	PLILKILHWPOLRMLPADIAFAVRALCCERARARALAAADPRGEGCSIAWRIA	120
121	LAQGRAAHTLHIGSRRTFSYSEERESNDAARAFILALCWDWGDGDSGSGSAGER	180
121	LAQGRAAHTLHIGSRRTFSYSEERESNDAARAFILALCWDWGDGDSGSGSAGER	180
181	APGAGDAAGSAGAEFGAGDGAAGGAAAPLSAGATVALLPAGPEPLTWGLARGR	240
181	APGAGDAAGSAGAEFGAGDGAAGGAAAPLSAGATVALLPAGPEPLTWGLARGR	240
241	TAVPTALRRGPIHCLRSAGARALVLAPEFESLEPDLPALRAMGLHMAAGPTHPAG	300
241	TAVPTALRRGPIHCLRSAGARALVLAPEFESLEPDLPALRAMGLHMAAGPTHPAG	300
301	ISDLAEVSAEVNVPVGYLSSPOSTTDCYITFSGTGLKKAISHLKLCCGFPQ	360
301	ISDLAEVSAEVNVPVGYLSSPOSTTDCYITFSGTGLKKAISHLKLCCGFPQ	360
361	LCGVHEDVLYLALPLHNSGSLGIIVGCMGIGATVILSKESAGQFWDCCQHRVTYQ	420
361	LCGVHEDVLYLALPLHNSGSLGIIVGCMGIGATVILSKESAGQFWDCCQHRVTYQ	420
421	YIGELCRYLVNPPSKERGHVRLAVSGLRPDWTFVRFPGLQVLETYGTENVA	480
421	YIGELCRYLVNPPSKERGHVRLAVSGLRPDWTFVRFPGLQVLETYGTENVA	480
481	TINYTGORGAVRASLYGHPFSLIRYDTVTGPIIDPOGHCATSPGEGGLVAAYS	540
481	TINYTGORGAVRASLYGHPFSLIRYDTVTGPIIDPOGHCATSPGEGGLVAAYS	540
541	QOSPFLGYAGPGLAOGKILKDVFPFGVFNTEGLLVCDDGFLRFDRDGTFRMAGE	600
541	QOSPFLGYAGPGLAOGKILKDVFPFGVFNTEGLLVCDDGFLRFDRDGTFRMAGE	600
601	NVAITEVAEVEFALPFLQEVNVYGVTVPGHGRAGMALVLRPPALDLMQYTHVSNL	660
601	NVAITEVAEVEFALPFLQEVNVYGVTVPGHGRAGMALVLRPPALDLMQYTHVSNL	660
661	PPYAPRFLRQESIAETETKQKVRMANSGFDSLSLPLVYLQAVGAYLPLTARY	720
661	PPYAPRFLRQESIAETETKQKVRMANSGFDSLSLPLVYLQAVGAYLPLTARY	720
721	SALLAGNRI 730	
721	SALLAGNRI 730	

[illegible]

Sequence Comparison ϵ^{-1}

Dd	974	TCACCTGTGGGCTGCAAGGCCAGAAACCAACCGTGTGAATFAGCAATTTGCTGGCTG	1033
Qy	978	AAAGTCCGCTGAAGTGAATGGGATGGGCCAGTGCACAGATACCTCTCTTCCGCCAGACATTA	1037
Dd	1034	AAAGTCCGCTGAAGTGAATGGGATGGGCCAGTGCACAGAAATCTCTTCCGCCAGACATTA	1093
Qy	1038	CAGACAGTGCCTGTACATCTTACCTCTGGGACACAGAGGCGCTCCCAAGGCTGTCCGA	1097
Dd	1094	CAGACAGTGCCTGTACATCTTACCTCTGGGACACAGAGGCGCTCCCAAGGCTGTCCGA	1153
Qy	1098	TCAGTCACTGAAAGATCTTGCAATGCGAAGGCTTCTATAGCTGTGTGTCTCACCAAG	1157
Dd	1154	TCAGTCACTGAAAGATCTTGCAATGCGAAGGCTTCTATAGCTGTGTGTCTCACCAAG	1213
Qy	1158	AAAGTGTGATCTACCTTCGCGCTCCCACTCTAACACATGTCCGGTTCCCTGCTGGCATGG	1217
Dd	1214	AAAGTGTGATCTACCTTCGCGCTCCCACTCTAACACATGTCCGGTTCCCTGCTGGCATGG	1273
Qy	1218	TGGACTCATAGGAGATTTGGGGCCACAGTGTGTCTGAATTCGAATTCGAGCTGTCACT	1277
Dd	1274	TGGACTCATAGGAGATTTGGGGCCACAGTGTGTCTGAATTCGAATTCGAGCTGTCACT	1333
Qy	1278	TCTGGGAAATTTGCCAGACACACAGGGTGAAGGTTCCTTCCAGTACATTTGGGGAGCTGTGCC	1337
Dd	1334	TCTGGGAAATTTGCCAGACACACAGGGTGAAGGTTCCTTCCAGTACATTTGGGGAGCTGTGCC	1393
Qy	1338	GATACCTTGTCAACCAAGCCGCCAGACAGACAGTGTGCATTAAGTCCGGCTGGCAG	1397
Dd	1394	GATACCTTGTCAACCAAGCCGCCAGACAGACAGTGTGCATTAAGTCCGGCTGGCAG	1453
Qy	1398	TGGCAGCGGGCTGCGCCAGATTCCTGGGAGGCTTTGTGCGGCGCTTCGGGCGCCCTGC	1457
Dd	1454	TGGCAGCGGGCTGCGCCAGATTCCTGGGAGGCTTTGTGCGGCGCTTCGGGCGCCCTGC	1513
Qy	1458	AGGTGCTGGAGACATATGGACTGACACAGGGCAACTGGCCACCATCACTACACAGAC	1517
Dd	1514	AGGTGCTGGAGACATATGGACTGACACAGGGCAACTGGCCACCATCACTACACAGAC	1573
Qy	1518	AGCGGGGCGCTGTGGGGCGTCTTCTTGAGCTTACAGCATATTTCCCTCTCTCTGA	1577
Dd	1574	AGCGGGGCGCTGTGGGGCGTCTTCTTGAGCTTACAGCATATTTCCCTCTCTCTGA	1633
Qy	1578	TTCCGTATGATGTCACACAGAGAGGCCAATTCGGAGACCCCAAGGACACTGTATGGCA	1637
Dd	1634	TTCCGTATGATGTCACACAGAGAGGCCAATTCGGAGACCCCAAGGACACTGTATGGCA	1693
Qy	1638	CATCTCCAGTGAAGCCAGGCGTGTGTGTGAGCCCGGTAAGCCAGCAGTCCCATTTCTGG	1697
Dd	1694	CATCTCCAGTGAAGCCAGGCGTGTGTGTGAGCCCGGTAAGCCAGCAGTCCCATTTCTGG	1753
Qy	1698	GCTATGCTGGCGGGCCAGAGCTGGGCCAGGGGAAAGTTGCTAAAGATGTCTTCGGGCTG	1757
Dd	1754	GCTATGCTGGCGGGCCAGAGCTGGGCCAGGGGAAAGTTGCTAAAGATGTCTTCGGGCTG	1813
Qy	1758	GGGATTTTTCTTCAACACTGGGAGCCTGCTGTCTGTGATGACCAAGTTTTCTCGCT	1817
Dd	1814	GGGATTTTTCTTCAACACTGGGAGCCTGCTGTCTGTGATGACCAAGTTTTCTCGCT	1873
Qy	1818	TCATATATCTTACTGGAGACACTTCTCAGTGGAAAGGGGGAATGTGGGCCAACCCAGG	1877
Dd	1874	TCATATATCTTACTGGAGACACTTCTCAGTGGAAAGGGGGAATGTGGGCCAACCCAGG	1933
Qy	1878	TGGCAGAAGTCTCGAGGCGCTAGATTTTCTTCAAGAGGTGAACGTCTATGGAAGTCACTG	1937
Dd	1934	TGGCAGAAGTCTCGAGGCGCTAGATTTTCTTCAAGAGGTGAACGTCTATGGAAGTCACTG	1993
Qy	1938	TGGCAGGCGCATGAAGCCAGGCTGGAATGACAGCCTTAGTTCGTGGTCCCCCGCAGCTT	1997
Dd	1994	TGGCAGGCGCATGAAGCCAGGCTGGAATGACAGCCTTAGTTCGTGGTCCCCCGCAGCTT	2053
Qy	1998	TGGACCTTATGACGCTCTACACCAACGATCTGAGAACTTGGCACTTATGCCCAGGCC	2057
Dd	2054	TGGACCTTATGACGCTCTACACCAACGATCTGAGAACTTGGCACTTATGCCCAGGCC	2113

Sequence Comparison

us-10-030-226-1.rng

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QY 2058 GATTCTAGAGCTCCAGAGTCTTTGCGCAGCAGAGACTTCAAGCAGGAAAGTTC 2117
DB 2114 GATTCTAGAGCTCCAGAGTCTTTGCGCAGCAGAGACTTCAAGCAGGAAAGTTC 2173
QY 2118 GGATGGCAATAGAGGCTTCAGACCCAGCAGCAGCAGTGTACCACTGTGAGTTCGACC 2177
DB 2174 GGATGGCAATAGAGGCTTCAGACCCAGCAGCAGCAGTGTACCACTGTGAGTTCGACC 2233
QY 2178 AGGCTGTAGTGTCTTACTCTCCCTTCACTCACTGCTGACAGCCCTTCTGCGAGGA 2237
DB 2234 AGGCTGTAGTGTCTTACTCTCCCTTCACTCACTGCTGACAGCCCTTCTGCGAGGA 2293
QY 2238 ACCTTCGATCTGAGAACTTCCACACTGAGGAGCAGCAGTGTGAGGAGTGG 2297
DB 2294 ACCTTCGATCTGAGAACTTCCACACTGAGGAGCAGCAGTGTGAGGAGTGG 2353
QY 2298 GGGCGGTTCAGGTGTACTGAGGAGTCTTCTATACCAAGTGGGCTCACT 2357
DB 2354 GGGCGGTTCAGGTGTACTGAGGAGTCTTCTATACCAAGTGGGCTCACT 2413
QY 2358 ATTGTGTATTAATGTGCTGAGAGCTGATCAGGTGTCTGACCTA 2404
DB 2414 ATTGTGTATTAATGTGCTGAGAGCTGATCAGGTGTCTGACCTA 2460

RESULT 8
ACD42510
ID ACD42510 standard; cDNA; 2574 BP.
AC ACD42510;
XX
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XX 09-SEP-2003 (first entry)
XX
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XX Novel human secreted and transmembrane protein PRO703 cDNA.
XX
XX Human; secreted and transmembrane protein; PRO; virulence; gene therapy;
XX
XX cell death; growth induction cascade; blood coagulation cascade;
XX
XX viral infection; gene; ss.
XX
XX Homo sapiens.
XX
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XX US2003050239-A1.
XX
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XX 13-MAR-2003.
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XX 15-OCT-2001; 2001US-00978191.
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XX 17-OCT-1997; 97US-0062250P.
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XX 03-NOV-1997; 97US-0064249P.
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XX 13-NOV-1997; 97US-0065311P.
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PR 13-MAY-1998; 98US-0085323P.
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PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
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PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
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PR 15-MAY-1998; 98US-0085597P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 26-MAY-1998; 98US-0087098P.
PR 26-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 28-MAY-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100036P.
PR 07-OCT-1998; 98US-00168978.
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AA24054
ID AA24054 standard; protein; 730 AA.
XX
AC AA24054;
XX
DT 25-JAN-2001 (first entry)
XX
DS Human PRO703 protein sequence SEQ ID NO:29.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
XX
KW tumourigenesis; detection; neoplastic cell growth; proliferation;
XX
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
XX
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN W0200053754-A1.

Sequence
Comparison
"D"

XX 14-SEP-2000.
XX 06-JAN-2000; 2000MO-US000277.
XX 08-MAR-1999; 99MO-US005028.
XX 12-MAR-1999; 99US-012357B.
XX 23-MAR-1999; 99US-0126773B.
XX 21-APR-1999; 99US-0130232B.
XX 23-APR-1999; 99US-0131445B.
XX 05-OCT-1999; 99MO-US023089.
XX 30-NOV-1999; 99MO-US028313.
XX 02-DEC-1999; 99MO-US028564.
XX 02-DEC-1999; 99MO-US031243.
XX 30-DEC-1999; 99MO-US031274.
XX
XX (GENE) GENETECH INC.
XX Baker K, Desauvage F, Goddard A, Gurney AL, Klein RD, Roy MA;
XX Wood W;
XX WPI; 2000-572269/53.
XX N-PSDB; AAC58239.
XX
XX New isolated antibody for use in compositions and methods for the
XX diagnosis and treatment of neoplastic cell growth and proliferation in
XX mammals, including humans, and in monitoring tumor treatment.
XX
XX Claim 61; Fig 29; 195BP; English.
XX
XX The present invention describes an isolated antibody (Ab) that binds to
XX one of the human proteins (p) designated PRO213, PRO1330, PRO1449,
XX PRO327, PRO324, PRO351, PRO362, PRO615, PRO538, PRO3664, PRO618,
XX PRO772, PRO703, PRO792 or PRO744. The Ab can be used in compositions and
XX methods for the diagnosis and treatment of neoplastic cell growth and
XX proliferation in mammals, including humans. Genes and polypeptides
XX encoded by them, that are amplified in the genome of a tumor cell, can
XX be identified and are useful targets for the treatment and prevention of
XX certain cancers and may be used to monitor tumor treatment. Compounds
XX that inhibit the expression or activity of the identified polypeptides,
XX can be identified and used as antagonists. Benign or malignant tumours,
XX inflammatory disorders and immunological disorders can be treated.
XX AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
XX in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
XX AAC58241 to AAC58245 represent human PRO polynucleotide and protein
XX sequences given in the exemplification of the present invention
XX
XX Sequence 730 AA;
XX
XX Query Match 100.0%; Score 3843; DB 3; Length 730;
XX Best Local Similarity 100.0%; NC 0;
XX Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCCCTATAPKPKKSGQLERJALGPRKSSGMSGMMQTPYERAGSMALLPILLIT 60
DB 1 MGCCCTATAPKPKKSGQLERJALGPRKSSGMSGMMQTPYERAGSMALLPILLIT 60
QY 61 PILLITGLHMPQLRMLPADLAFVAVRACCKRLARALAAAAADPEEGCSLAWLLAE 120
DB 61 PILLITGLHMPQLRMLPADLAFVAVRACCKRLARALAAAAADPEEGCSLAWLLAE 120
QY 131 LAOGRRAATPLIHGSRPFYSFARERENPAAAFALGMDGPDGDSGEGSAGEGERA 180
DB 131 LAOGRRAATPLIHGSRPFYSFARERENPAAAFALGMDGPDGDSGEGSAGEGERA 180
QY 181 APGGGAAAGSGAFAGCGAGGAAAGGAAAPLSPGATVALLPAGCEELTMVGLAKKGR 240
DB 181 APGGGAAAGSGAFAGCGAGGAAAGGAAAPLSPGATVALLPAGCEELTMVGLAKKGR 240
QY 241 TAFVPTALRGPFLHGLRSCGALVLAPEFESLEEDPPLRPMAGMLMAAGPTPDAG 300
DB 241 TAFVPTALRGPFLHGLRSCGALVLAPEFESLEEDPPLRPMAGMLMAAGPTPDAG 300
QY 300 TAFVPTALRGPFLHGLRSCGALVLAPEFESLEEDPPLRPMAGMLMAAGPTPDAG 300
DB 300 TAFVPTALRGPFLHGLRSCGALVLAPEFESLEEDPPLRPMAGMLMAAGPTPDAG 300

226-2.rag

Sequence
Comparison "D" Page 4

QY 301 ISDLAENSAEVDGPVPGVSSPSTIDPCLYFTSGTGPKAARISHKILQCCGEPVQ 360
DB 301 ISDLAENSAEVDGPVPGVSSPSTIDPCLYFTSGTGPKAARISHKILQCCGEPVQ 360
QY 361 LQGHQEDVYIALPYHMSGLGIVGCMGIGATVTLKSKFSAGQWMECCQGHVTVFQ 420
DB 361 LQGHQEDVYIALPYHMSGLGIVGCMGIGATVTLKSKFSAGQWMECCQGHVTVFQ 420
QY 421 YIGELCRVLYVQPPSKAERGHKRLAVAGSLRPTMERFVRFGFLQVETVGLTEGVA 480
DB 421 YIGELCRVLYVQPPSKAERGHKRLAVAGSLRPTMERFVRFGFLQVETVGLTEGVA 480
QY 481 TINYTGORGAVGRASMLYKHIFPFSILRDVVTGEPIDPQCHCATSPCEGLVAPVS 540
DB 481 TINYTGORGAVGRASMLYKHIFPFSILRDVVTGEPIDPQCHCATSPCEGLVAPVS 540
QY 541 QOSPFYVAGGFEIACQKLDKDFRDPDVFPTGDLVCDQGFARFHDRTDTRFWKGE 600
DB 541 QOSPFYVAGGFEIACQKLDKDFRDPDVFPTGDLVCDQGFARFHDRTDTRFWKGE 600
QY 601 NVATTEVAEVEALDFQEVNNGVTVPGHEGRAGMALVLRPPALDLMQLYTVEENT 660
DB 601 NVATTEVAEVEALDFQEVNNGVTVPGHEGRAGMALVLRPPALDLMQLYTVEENT 660
QY 661 PPVAPRPRFLQESLATTETFPQOKRMANEGFPSTLSDPVLVDQAVAPLPTTARY 720
DB 661 PPVAPRPRFLQESLATTETFPQOKRMANEGFPSTLSDPVLVDQAVAPLPTTARY 720
QY 721 SALLAGNINI 730
DB 721 SALLAGNINI 730

RESULT 4
AA24054 standard; protein; 730 AA.
AA24054;
24-APR-2001 (first entry)
Human fatty acid transporter P98C67.
Human, fatty acid transporter; P98C67; long-chain fatty acid uptake;
oleic acid; drug screening; gene therapy; metabolic disorder;
cardiomyopathy; skeletal muscle disorders; renal failure.
Homo sapiens.
W0200104301-A1.
18-JAN-2001.
07-JUL-2000; 2000MO-JP004549.
08-JUL-1999; 99AP-00194179.
18-OCT-1999; 99US-0155866P.
25-APR-2000; 2000UP-00128993.
(HELI-) HELIX RES INST.
Morikawa N, Masuno Y, Ota T, Isogai T, Nishikawa T, Kawai Y;
WPI; 2001-138349/14.
N-PSDB; AAF27417.
Fatty acid transporter protein and encoded gene P98C67 cloned from human
cDNA library, with activity of oleic acid incorporation, useful as target
molecule of preventives or remedies of fatty-acid metabolic disorders.
Claim 1; Page 48-51; 58bp; Japanese.

Sequence Comparison

RESULT 3

088561 PRELIMINARY; PRT; 614 AA.
 ID 088561
 AC 088561
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Fatty acid transport protein 3 (PATP3) (long-chain fatty acid transport protein 3) (Fragment).
 GN SLC27A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=88337365; PubMed=9671728;
 RA Hirsch D., Stahl A., Lodish H.F.;
 RT "A family of fatty acid transporters conserved from mycobacterium to man".
 RT Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629 (1998).
 CC -1- FUNCTION: INVOLVED IN TRANSLATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR TRIGLYCERIDE SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
 CC -1- TISSUE SPECIFICITY: LUNG, LIVER, AND TESTIS.
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; AF072158; AAC40187.1; -.
 DR MGD; MGI:1347358; SLC27A3.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0006869; F: lipid transport; IEA.
 DR GO; GO:0008152; P: metabolism; IEA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 2.
 DR PROSITE; PS00455; AMP BINDING; 1.
 DR GlycoProtein; Lipid transport; Transmembrane; Transport.
 KM NON TER 1
 FT TRANSMEM 99 119 POTENTIAL.
 FT TRANSMEM 262 282 POTENTIAL.
 FT CARBOHYD 367 367 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 614 AA; 67041 MW; 332A558CDP969 CRC64;

Query Match 71.9%; Score 2763; DB 11; Length 614;
 Best Local Similarity 83.5%; Pred. No. 1,5e-181;
 Matches 526; Conservative 35; Mismatches 53; Indels 16; Gaps 2;
 QY 101 AADPDPGGGCGGLARLAAGQRAAHPLTHSRPFSYSEAESESRRAARAFALGWM 160
 DB 1 AADPDPGGGCGGLARLAAGQRAAHPLTHSRPFSYSEAESESRRAARAFALGWM 60
 QY 161 DWGPDPGGGSGSAGSRRAAPGAGDAAGCAEFAAGDGAARAGGAAPLSGATVALL 220
 DB 61 TGGRRG--SGRSGTSGARVAPPGDAAA-----RRTTPPLAAGAVALL 104
 QY 221 LPAGPEFLMPLFGLAAGLRTAFPTALRRGPLHLCLSCGAPALVAFEPLESLPPLP 280
 DB 105 LPAGPEFLMPLFGLAAGLRTAFPTALRRGPLHLCLSCGAPALVAFEPLESLPPLP 164
 QY 281 ALRAGLHLMAAGPPTGAGISDLAEVASAEVDGPGVGLYSPOSITDTCLYFTSGTTG 340
 DB 165 ALRAGLHLMAAGPPTGAGISDLAEVASAEVDGPGVGLYSPOSITDTCLYFTSGTTG 224
 QY 341 LFKARISHLKLQCCGFYHLCGVHEDVYIALPLTHMGSLGLGVCGMIGATVVLKS 400
 DB 225 LFKARISHLKLQCCGFYHLCGVHEDVYIALPLTHMGSLGLGVCGMIGATVVLKP 284
 QY 401 KFSAGQWEDCGQHRVTFQYIGELCRYLVNPPSKAEKRGKRVLAAGSGLRPDTWEFV 460
 DB 285 KFSAGQWEDCGQHRVTFQYIGELCRYLVNPPSKAEKRGKRVLAAGSGLRPDTWEFV 244

QY 461 RERGPLQVLEVTGLTEGNATINYTGORGAVGRASMTLYKHIFPFLRYDVTGPIRDE 520
 DB 345 RERGPLQVLEVTGLTEGNATINYTGORGAVGRASMTLYKHIFPFLRYDVTGPIRDE 404
 QY 521 QGHCMATSPPEBPLVAVPVSQSPFLGVAGGPELLOCKLKDVPFPGVFPNGLDLYCD 580
 DB 405 QGHCMATSPPEBPLVAVPVSQSPFLGVAGGPELLOCKLKDVPFPGVFPNGLDLYCD 464
 QY 581 QGHCMATSPPEBPLVAVPVSQSPFLGVAGGPELLOCKLKDVPFPGVFPNGLDLYCD 640
 DB 465 QGHCMATSPPEBPLVAVPVSQSPFLGVAGGPELLOCKLKDVPFPGVFPNGLDLYCD 524
 QY 641 LRPPEALDLMLQYTHVSNLEPPVAPRPLRLQESLATTETPQCKVRANEGFDPSTLSD 700
 DB 525 LRPPEALDLMLQYTHVSNLEPPVAPRPLRLQESLATTETPQCKVRANEGFDPSTLSD 584
 QY 701 PLYVIDQAVGAYPLPTTARYSALLAGNTRI 730
 DB 585 PLYVIDQAVGAYPLPTTARYSALLAGNTRI 614

RESULT 4

088K70 PRELIMINARY; PRT; 446 AA.
 ID 088K70
 AC 088K70
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Solute carrier family 27.
 GN SLC27A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=2254683; PubMed=12466851;
 RA "The Riken Genome Consortium".
 RA "Analysis of the mouse transcriptome based on functional annotation of the Riken Genome Consortium".
 RT 60,770 full-length cDNAs.
 RT Nature 420:563-573 (2002).
 DR EMBL; AK076014; BAC36120.1; -.
 DR MGD; MGI:1347358; SLC27A3.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0008152; P: metabolism; IEA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP BINDING; 1.
 SQ SEQUENCE 446 AA; 49317 MW; BALED75849EDF92B CRC64;

Query Match 54.7%; Score 2103; DB 11; Length 446;
 Best Local Similarity 87.9%; Pred. No. 2.3e-136;
 Matches 392; Conservative 26; Mismatches 28; Indels 0; Gaps 0;
 QY 285 MGLHMAAGPPTGAGISDLAEVASAEVDGPGVGLYSPOSITDTCLYFTSGTTGAPKA 344
 DB 1 MGLHMAAGPPTGAGISDLAEVASAEVDGPGVGLYSPOSITDTCLYFTSGTTGAPKA 60
 QY 345 ARISHLKLQCCGFYHLCGVHEDVYIALPLTHMGSLGLGVCGMIGATVVLKSKSA 404
 DB 61 ARISHLKLQCCGFYHLCGVHEDVYIALPLTHMGSLGLGVCGMIGATVVLKSKSA 120
 QY 405 GQFPEWCGQHRVTFQYIGELCRYLVNPPSKAEKRGKRVLAAGSGLRPDTWEFVRFG 464
 DB 121 GQFPEWCGQHRVTFQYIGELCRYLVNPPSKAEKRGKRVLAAGSGLRPDTWEFVRFG 180
 QY 465 PLYVIDQAVGAYPLPTTARYSALLAGNTRI 730
 DB 181 PLYVIDQAVGAYPLPTTARYSALLAGNTRI 614